GLOBAL TASK FORCE ON
CHOLERA CONTROL

EPIDEMIOLOGY OF THE 7TH WAVE CHOLERA PANDEMIC IN SUB-SAHARAN AFRICA

What Can Genomic Data Tell Us?

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AIM

To understand the epidemiology of cholera in light of genomic data on *V. cholerae.*

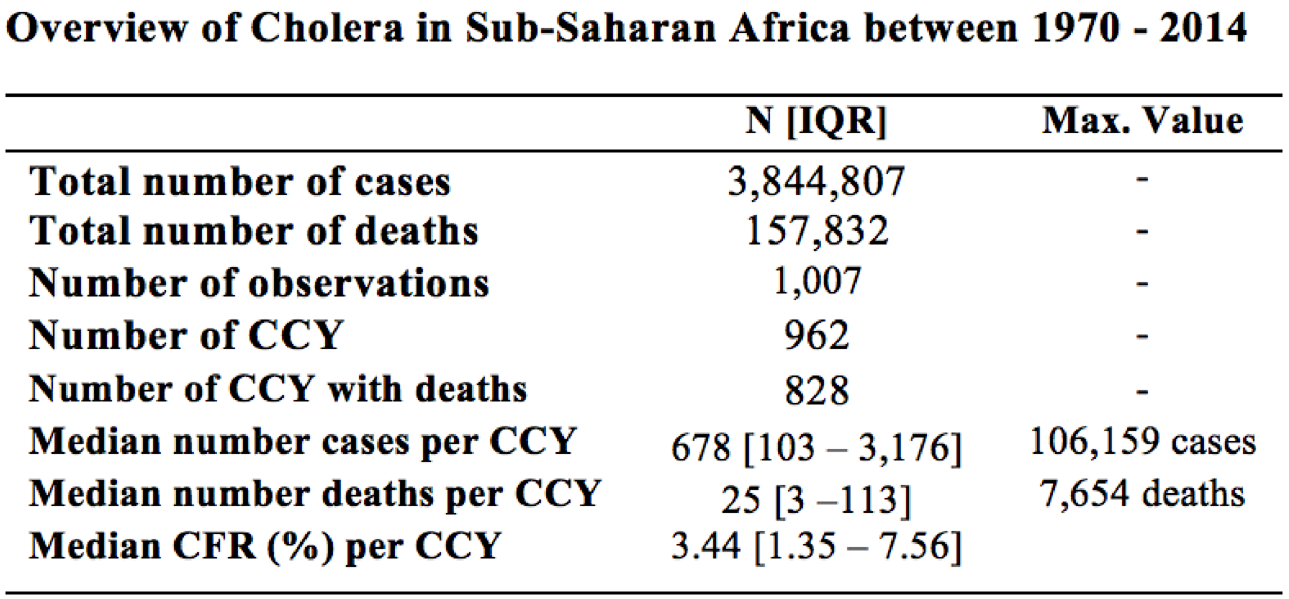
To share preliminary findings, gaps in the available epi and genomic data, and possible next steps.

OVERVIEW OF CHOLERA IN SUB-SAHARAN AFRICA BETWEEN 1970 - 2014

WHO reported cholera data

- Global Health Observatory
- Weekly Epidemiological Records

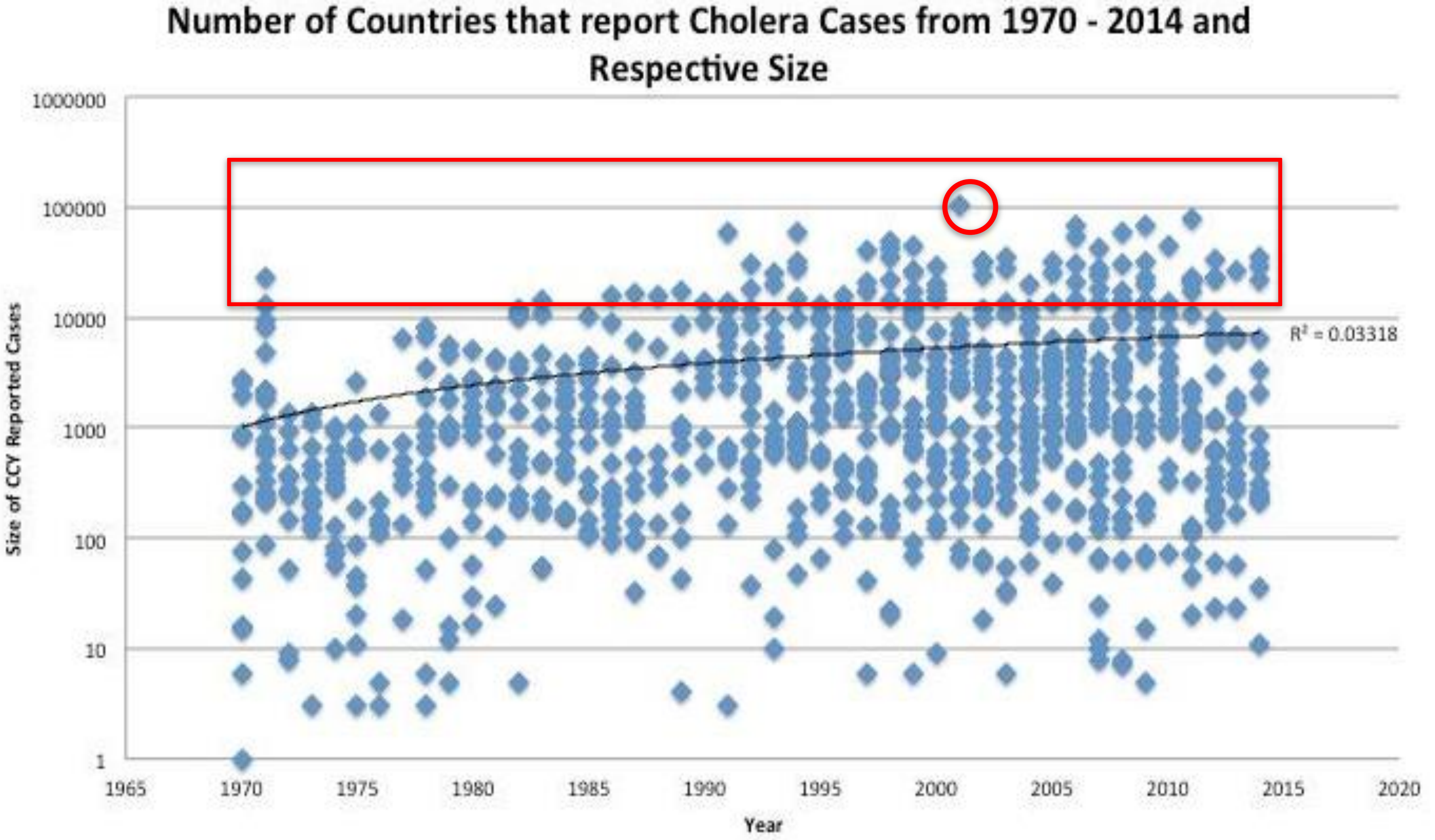
Cholera-country year (CCY)



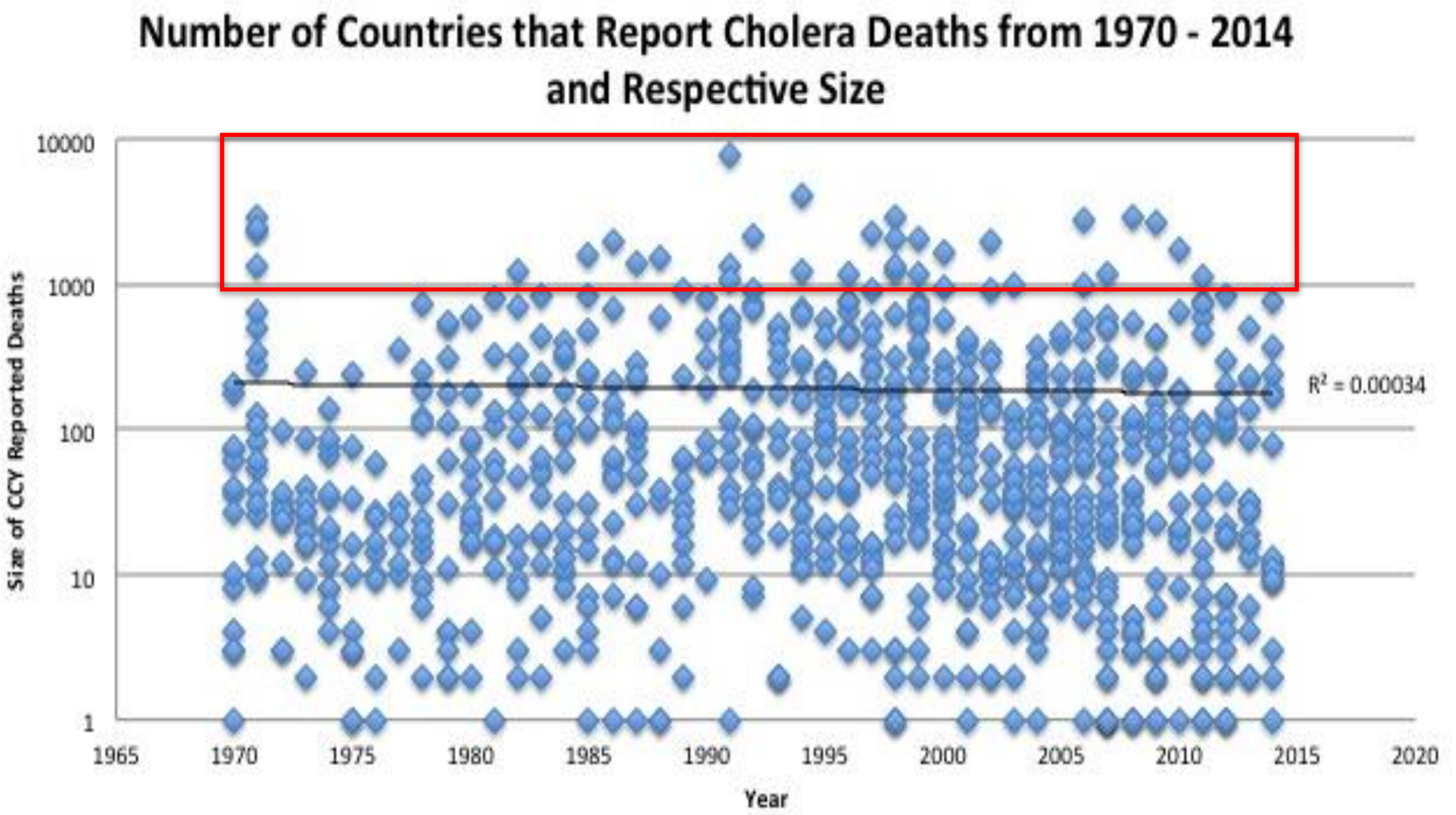
Overview of Cholera in Sub-Saharan Africa between 1970 - 2014

	N [IQR]	Max. Value
Total number of cases	3,844,807	-
Total number of deaths	157,832	-
Number of observations	1,007	-
Number of CCY	962	-
Number of CCY with deaths	828	-
Median number cases per CCY	678 [103 – 3,176]	106,159 cases
Median number deaths per CCY	25 [3 –113]	7,654 deaths
Median CFR (%) per CCY	3.44 [1.35 – 7.56]	

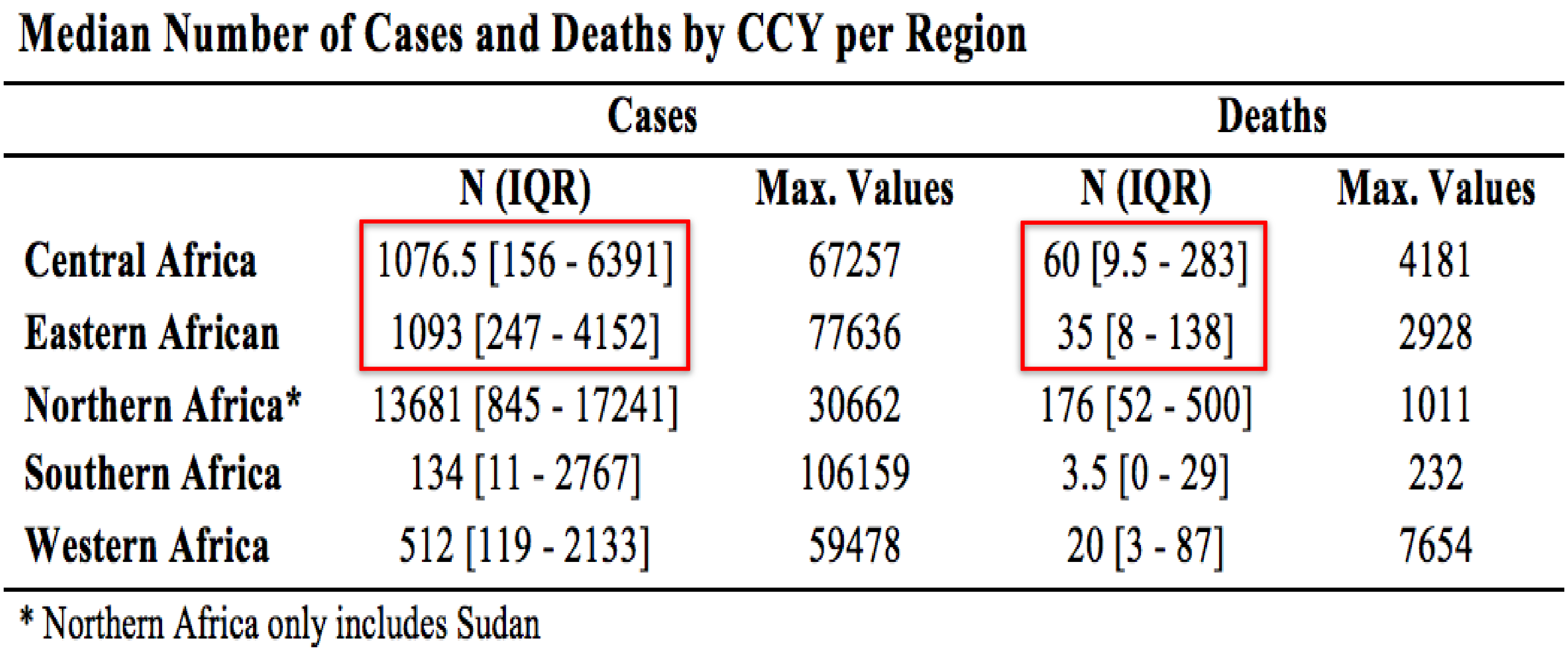
50 CCY'S REPORT OVER 20,000 CASES



32 CCY'S REPORT OVER 1,000 DEATHS



CENTRAL AND EASTERN AFRICA EXPERIENCE HIGHER MEDIAN CHOLERA DEATHS



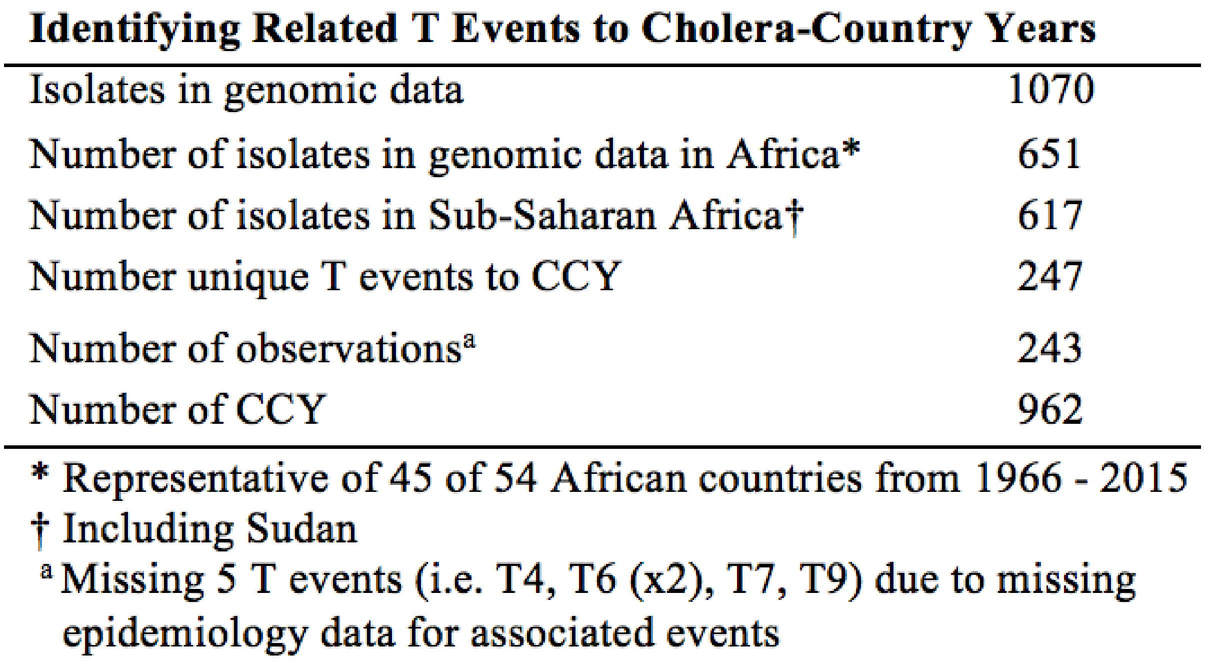
Median Number of Cases and Deaths by CCY per Region

	Cases		Deaths	
	N (IQR)	**Max. Values**	**N (IQR)**	**Max. Values**
Central Africa	1076.5 [156 - 6391]	67257	60 [9.5 - 283]	4181
Eastern African	1093 [247 - 4152]	77636	35 [8 - 138]	2928
Northern Africa*	13681 [845 - 17241]	30662	176 [52 - 500]	1011
Southern Africa	134 [11 - 2767]	106159	3.5 [0 - 29]	232
Western Africa	512 [119 - 2133]	59478	20 [3 - 87]	7654

* Northern Africa only includes Sudan

AVAILABLE GENOMIC ISOLATE DATA REPRESENTS A QUARTER OF CCY’S.

- Wiell et al. “Genomic History of the Seventh Pandemic of Cholera in Africa.” Science. 2017
- T Events – single expanded lineage



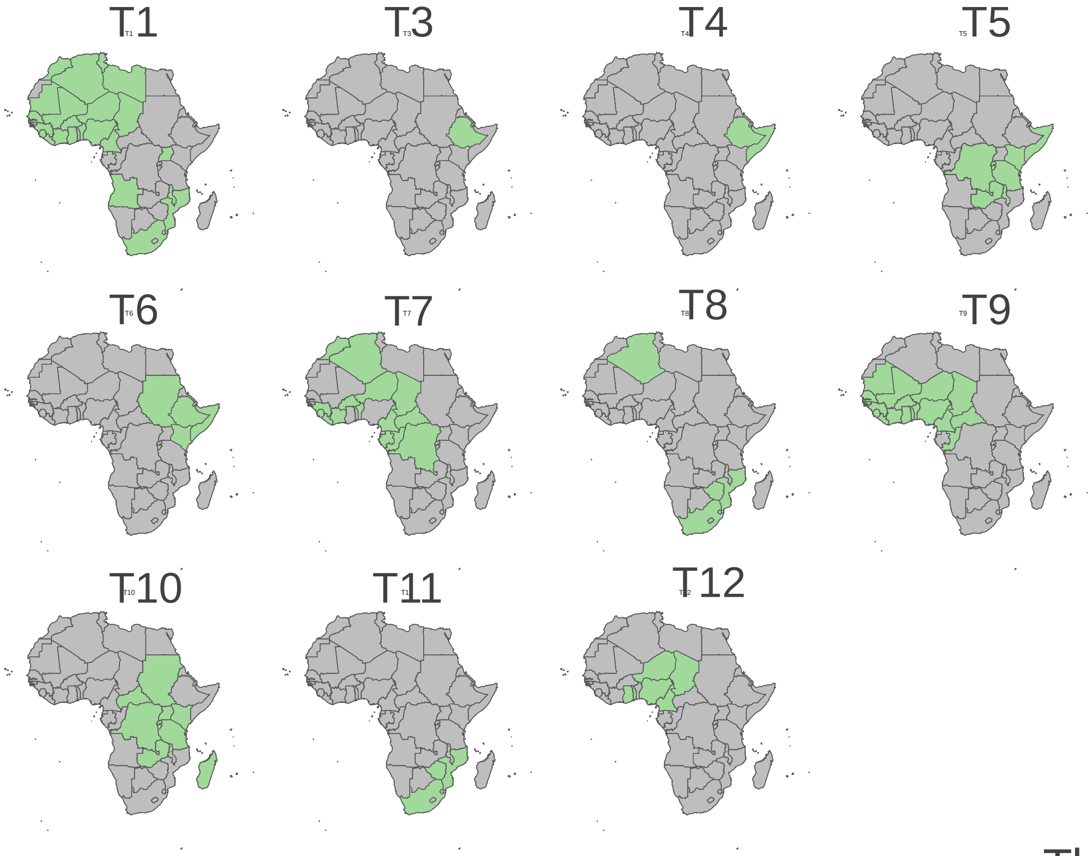
Identifying Related T Events to Cholera-Country Years	
Isolates in genomic data	1070
Number of isolates in genomic data in Africa*	651
Number of isolates in Sub-Saharan Africa†	617
Number unique T events to CCY	247
Number of observations[a]	243
Number of CCY	962

* Representative of 45 of 54 African countries from 1966 - 2015

† Including Sudan

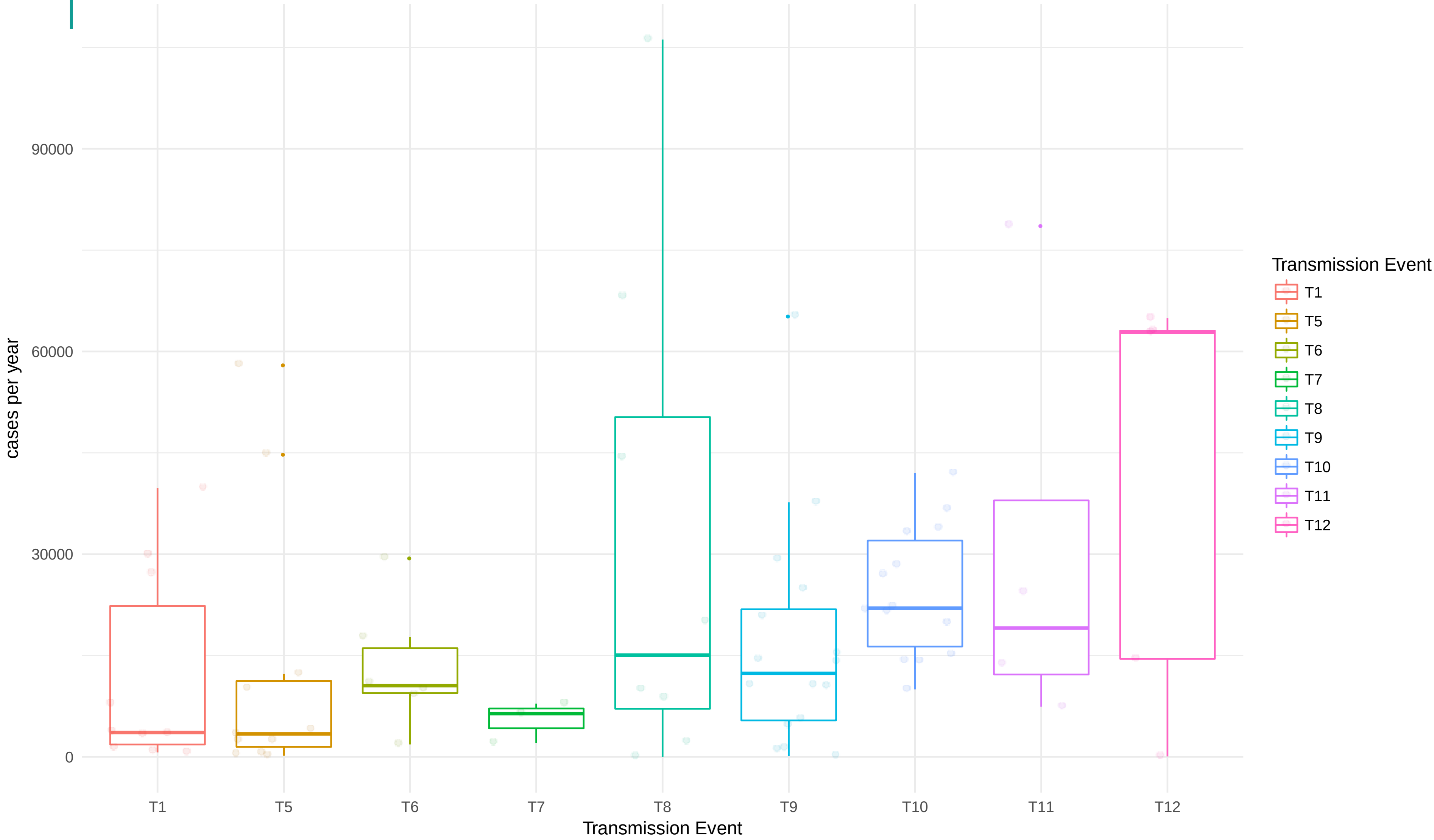
[a] Missing 5 T events (i.e. T4, T6 (x2), T7, T9) due to missing epidemiology data for associated events

T1 HAS AFFECTED A REGION WITH THE GREATEST POPULATION (495 MILLION) FOLLOWED BY T9 (423 MILLION).

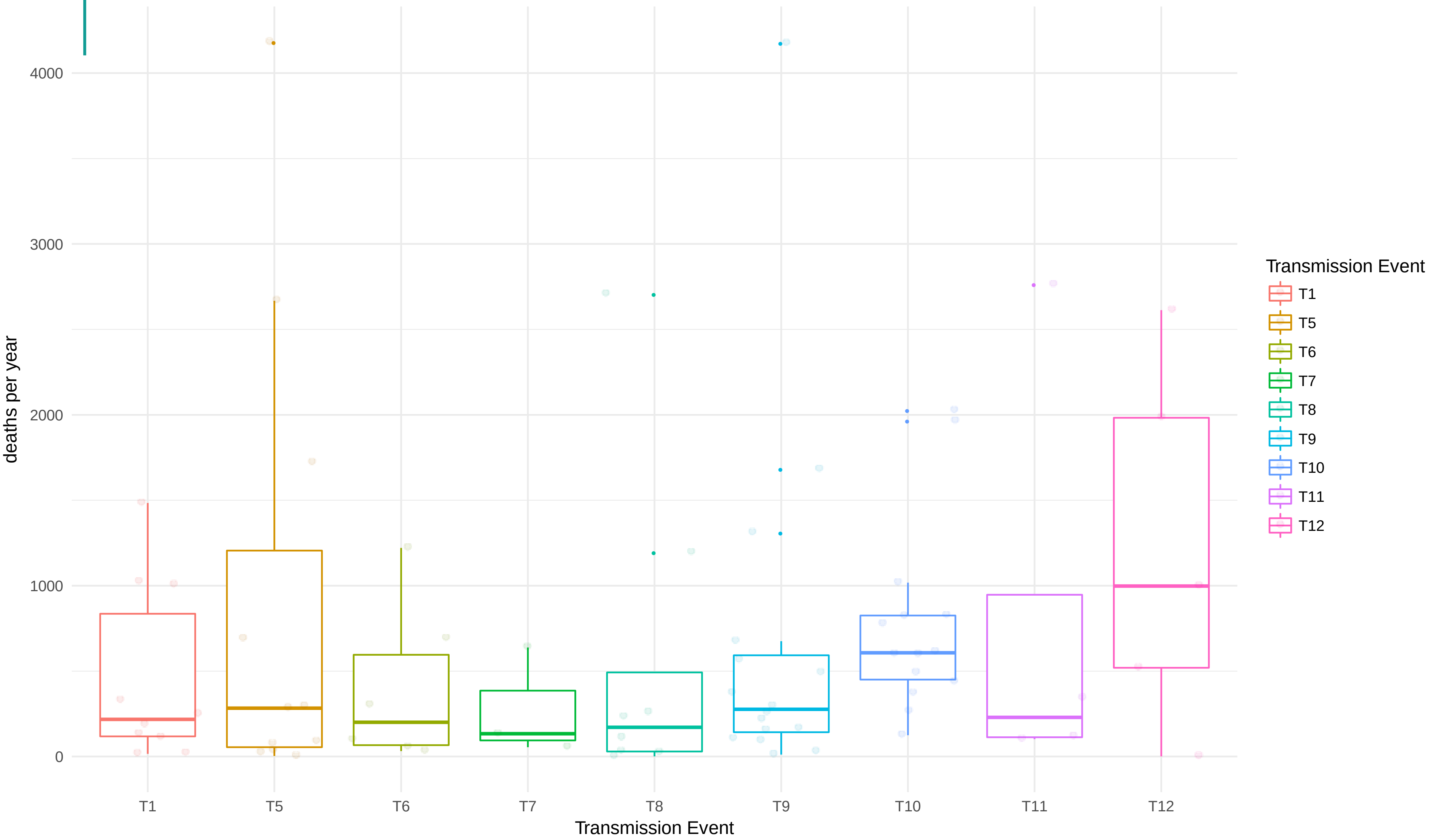


The World Bank 2016

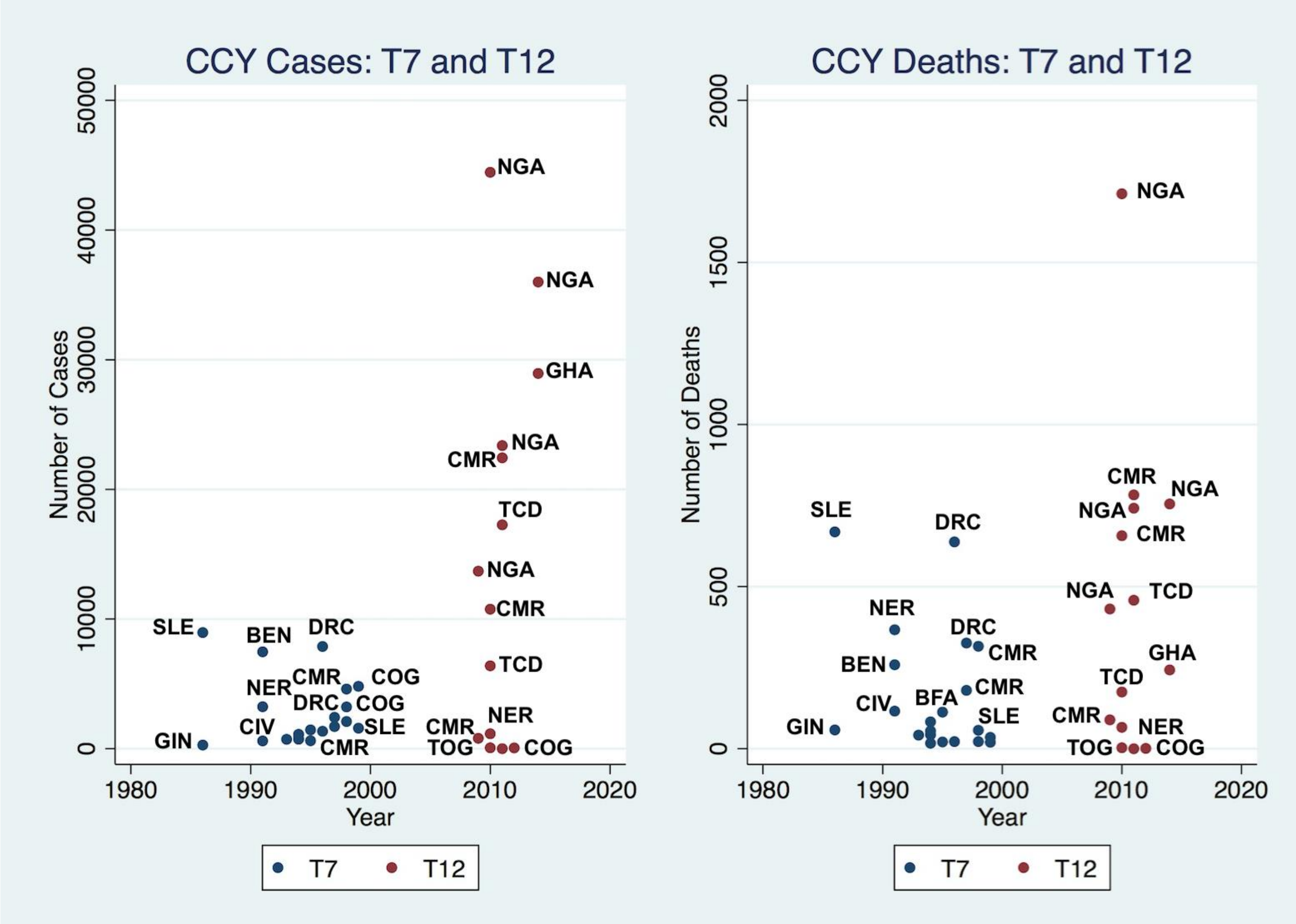
MEDIAN CASES PER YEAR BY T EVENTS VARY LESS THAN ANTICIPATED.



THE DIFFERENCE BETWEEN MEDIAN DEATHS PER YEAR IS LESS.

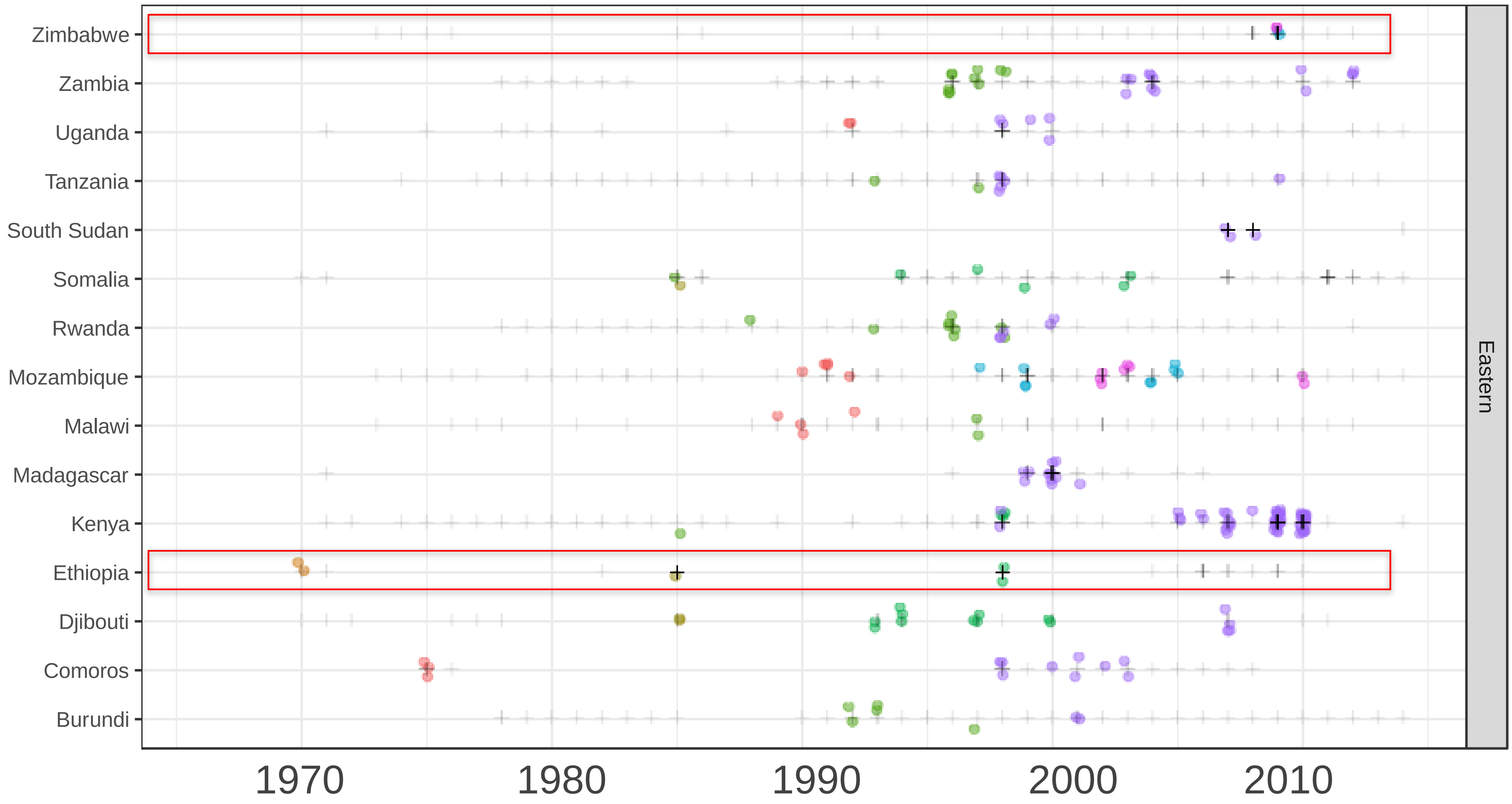


THE COUNTRIES AFFECTED MAY SKEW PERCEIVED IMPACT OF T.

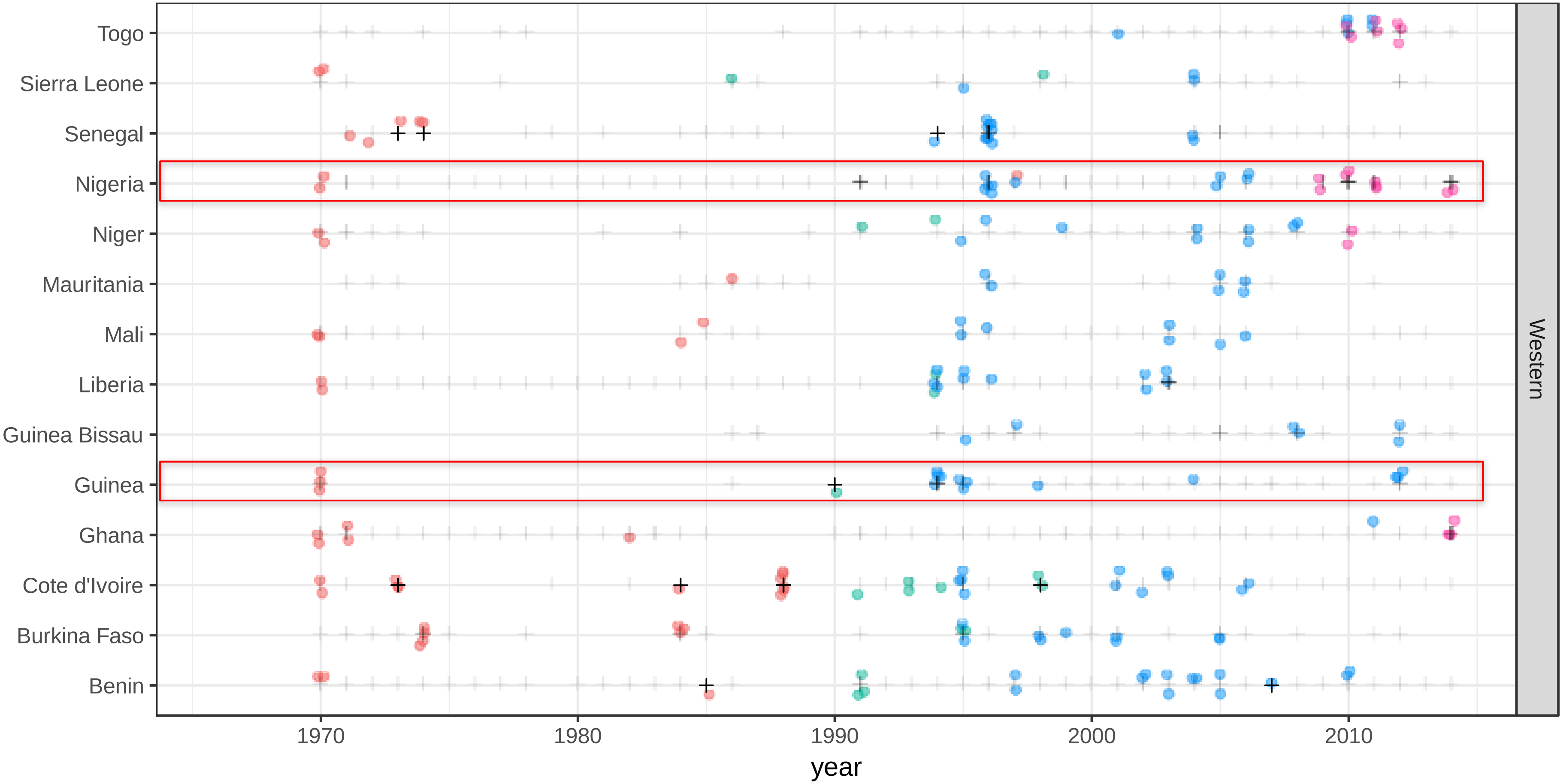


FILLING THE GAPS

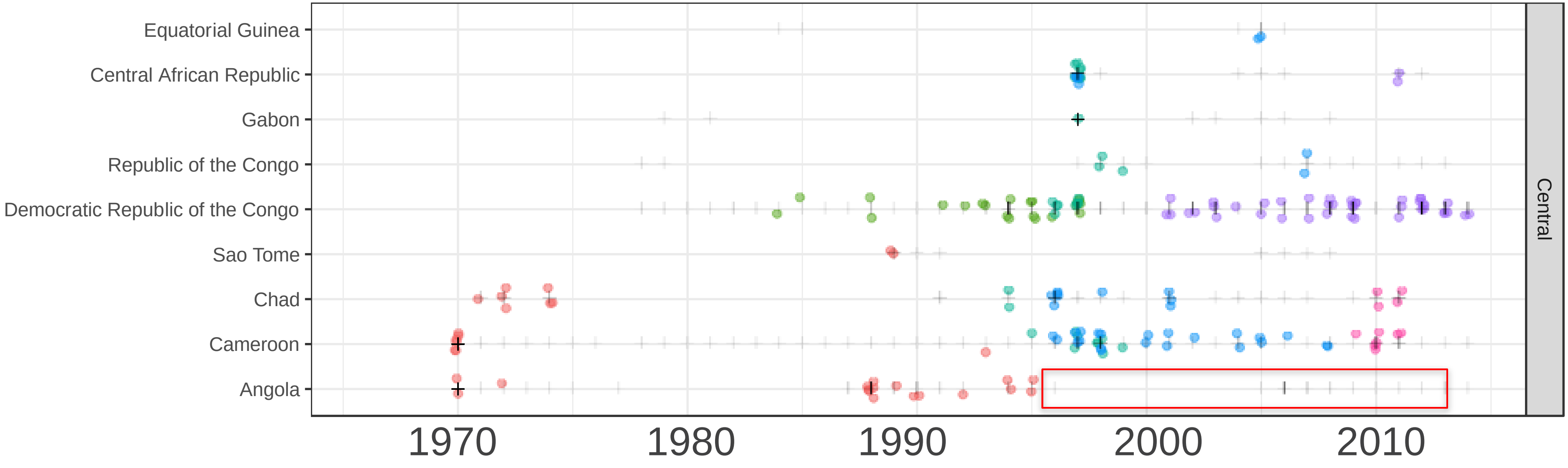
EASTERN AFRICA



WESTERN AFRICA



CENTRAL AFRICA



A ROBUST, EXPANDABLE GENOMIC REPOSITORY OF *V. CHOLERAE.*

- Identifying existing isolates that:
  - Have not been analysed.
  - Have been analysed but not yet published.
- Providing technical assistance for analyses and interpretation
- Modeling to address existing data gaps to better understand regional and global trends
- Establishing processes and SOPs to aid in systematic collection of isolates and genomic analyses, with the necessary meta-data included

QUESTIONS LEFT TO ANSWER

Are T’s the most meaningful way to assign lineage classes? Are there other ways?

Are there specific strains to watch out for?

What is the effect of the introduction of a new strain in a population?

How do we translate the appearance of a genomic strain or wave into prospective control action?

Can we detect the emergence of a new lineage and assess the risk of spread/introduction into Africa?

ACKNOWLEDGEMENTS

David Olson, MD

Andrew Azman, PhD

Francisco Luquero, MD, MPH

Dominique Legros, MD

The GTFCC Team

Reference:

Weill, François-Xavier ; Domman, Daryl ; Njamkepo, Elisabeth ; Tarr, Cheryl ; Rauzier, Jean ; Fawal, Nizar ; Keddy, Karen H ; Salje, Henrik ; Moore, Sandra ; Mukhopadhyay, Asish K ; Bercion, Raymond ; Luquero, Francisco J ; Ngandjio, Antoinette ; Dosso, Mireille ; Monakhova, Elena ; Garin, Benoit ; Bouchier, Christiane ; Pazzani, Carlo ; Mutreja, Ankur ; Grunow, Roland ; Sidikou, Fati ; Bonte, Laurence ; Breurec, Sébastien ; Damian, Maria ; Njanpop-Lafourcade, Berthe-Marie ; Sapriel, Guillaume ; Page, Anne-Laure ; Hamze, Monzer ; Henkens, Myriam ; Chowdhury, Goutam ; Mengel, Martin ; Koeck, Jean-Louis ; Fournier, Jean-Michel ; Dougan, Gordon ; Grimont, Patrick A D ; Parkhill, Julian ; Holt, Kathryn E ; Piarroux, Renaud ; Ramamurthy, Thandavarayan ; Quilici, Marie-Laure ; Thomson, Nicholas R. “Genomic history of the seventh pandemic of cholera in Africa.” Science (New York, N.Y.). 10 November 2017. Vol.358(6364). pp.785-789

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